Current Studies on Tick Biology in Relation to Disease in the Americas[1]

DANIEL E. SONENSHINE

Biology Department, Old Dominion College, Norfolk, Virginia 23508

In recent years, important new findings which have emerged from laboratory investigations on ticks have considerably increased our knowledge of the mechanisms involved in pathogen-vector-host interrelationships. Gregson (1960) described the structural organization of the mouthparts of the Rocky Mountain wood tick, *Dermacentor andersoni* Stiles, which facilitates the alternate salivation and ingestion of the saliva-host fluid mixtures. Yunker and Cory (1967) demonstrated the feasibility of culturing tick tissues in defined media and the growth of Colorado tick fever virus in the cultures for up to 166 days. More recently, Yunker and Rudbach (personal communication) used serological tests of the gut contents of ticks to identify the species of hosts upon which the ticks had fed. The development of this new laboratory technique may offer a means of exceeding the limitations of field sampling procedures requiring capture and direct examination of hosts. The feasibility of mass rearing permanently tagged ticks by means of transovarial transmission of radioisotopes has been demonstrated (Sonenshine and Yunker 1968). Knülle (1966) proved the presence of an atmospheric water sorption mechanism in the larvae of 3 American tick species. More recently, Knülle (personal communication) used tritium labeling to quantitate the rate of water exchange in the larvae of the American dog tick, *Dermacentor variabilis* (Say), in relation to its environment. Nathanson (1969) demonstrated the role of the epidermis as a water pump in the rabbit tick, *Haemaphysalis leporispalustris* (Packard), by electron microscopic studies of this organ. George (1964) described the circadian rhythm regulating dropoff of engorged rabbit ticks and its ecological value in maximizing the host-finding success of subsequent stages or generations.

These selected examples illustrate the rapid progress now current in the Americas in elucidating little-known biological mechanisms or development of new techniques that significantly affect knowledge of the vector efficiency of ticks and of their abundance. However, an important test of the value of the current and anticipated future progress is in its application to the tickborne disease focus. The advantages of the development of laboratory investigations in relation *to*, rather than separate *from* the investigations of the ecology of tickborne disease foci constitute the subject of this paper.

Watt (1966) and his co-workers described the advantages to be gained from the application of the methods of systems analysis to problems in ecology.

Mott (1966) contributing to the same work, discussed the way in which data can be accumulated and analyzed to determine the degree to which natural regulation is present in biological systems and to evaluate the roles of the several dominant variables that control it. This holistic approach focuses attention on the dominant deterministic variables and conceptually integrates them in a manner which describes the complex ecosystem within which the subject problem is contained. Ultimately, the analysis leads to the development of a hypothetical mathematical model which associates the dominant elements affecting the regulation of the vector or the vector-pathogen relationship. Although it suffers from the inherent risk of oversimplification, this defect is overshadowed by its immense advantage in predicting new biological information of importance in public health, military medicine, or conservation when only a few key variables are known. An example can be seen in the algebraic expression used by Watt (1966) where $I =$ rate of population change between generations, $Nn =$ number present at 1 generation, $Nn + 1 =$ number present at the beginning of the next generation, $Si =$ survival rate during the ith age interval, $P♀ =$ number of females, and $F =$ fecundity.

$$I = \frac{N_{n+1}}{N_n} = \left(\prod_{i=i}^{i=m} S_i \right) P♀ \cdot F$$

More recently, Curtis and Hill (1968), working on tsetse flies, developed deterministic equations to predict the probability of obtaining tsetse fly eradication in isolated populations by release of sterile males or flies bearing sterility chromosome translocations.

Deterministic equations and population models have long been used in studies of population dynamics. However, their application in studies on the ecology and/or epidemiology of tickborne diseases has been largely ignored. This is unfortunate, since hypothetical models, developed following the acquisition of suitable preliminary knowledge of the subject life history, can be used to guide the investigator and his project team in developing field plans and laboratory experiments which yield data of the type needed for the model equation. This process conserves available research energy and maximizes the value of each small bit of information obtained.

Rocky Mountain spotted fever is an example of a disease problem which may, perhaps, be amenable to this approach. Consideration is now being given to development of hypothetical mathematical models that may serve to integrate existing knowledge in a form that will yield maximum scientific benefit. Certain of the elements needed for this approach have been under investigation for several years, and knowledge